



OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. NCBI_TAXID=9606;
RA	SEQUENCE FROM N.A.
RA	"Antithrombotic Thrombin Variants";
RA	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL	EMBL; AY344794; AAR0143; 1; -.
DR	GO; GO:0005509; F:calcium ion binding; IEA.
DR	GO; GO:0004263; F:chymotrypsin activity; IEA.
DR	GO; GO:0003809; F:thrombin activity; IEA.
DR	GO; GO:0004295; F:trypsin activity; IEA.
DR	GO; GO:0007596; P:blood coagulation; IEA.
DR	GO; GO:0006508; P:proteinase and peptidolysis; IEA.
DR	INTERPRO; IPR01254; Peptidase_S1.
DR	INTERPRO; IPR01314; Peptidase_SIA.
DR	INTERPRO; IPR00903; Pept_Ser_Cys.
DR	PRAM; PF00089; TRYPSIN; 1.
DR	PRINTS; PR01505; CHYMOTRYPSIN.
DR	SMART; SM00020; TRYSP_SPC; 1.
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.
DR	PROSITE; PS00155; TRYPSIN_SER; 1.
DR	KW: Hydrolase; Protease; Serine protease.
FT	Hydrolase; Protease; Serine protease.
SQ	SEQUENCE 295 AA; 33637 MW; 7B531BC30738DB1 CRC64;
DR	Query Match 100.0%; Score 131; DB 2; Length 295; Best Local Similarity 100.0%; Pred. No. 1.4e-09; Mismatches 0; Indels 0; Gaps 0;
DR	Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DR	Db 224 AGYKPPDEGKRGDACEGDSGGFFV 246
DR	RESULT 4
DR	THRB_HUMAN
ID	THRB_HUMAN
STANDARD	PRT; 622 AA.
AC	P00754; 1986 (Rel. 01, Created)
DT	01-JAN-1990 (Rel. 13, Last sequence update)
DT	25-OCT-2004 (Rel. 45, Last annotation update)
DE	Prothrombin precursor (EC 3.4.21.5) (Coagulation factor III).
GN	Name=F2;
OS	Homo sapiens (Human).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhini; Hominidae; Homo. NCBI_TAXID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
DR	Degen S.J.F., Davie E.W.; MEDLINE=88077877; PubMed=2825773;
DR	RT "Nucleotide sequence of the gene for human prothrombin."; Biochemistry 26:6165-6177(1987).
DR	RN [2]
RP	SEQUENCE FROM N.A., AND VARIANT MTR-165.
DR	Rieder M.J., Armel T.Z., Carrington D.P., Chung M.-W., Lee K.L., Ozuna M., Poel C.L., Toth E.J., Yil Q., Nickerson D.A.; RT PHRC, Seattle, WA (URL: http://99a.gs.washington.edu)."; Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
RN	[3]
RP	SEQUENCE OF 8-622 FROM N.A.
DR	Degen S.J.F., McGillivray R.T.A., Davie E.W.; MEDLINE=83231469; PubMed=6305407;
DR	RT "Characterization of the complementary deoxyribonucleic acid and gene coding for human prothrombin."; Biochemistry 22:2087-2097(1983).
RN	[4]
RP	SEQUENCE OF 44-314.
DR	MEDLINE=7193964; PubMed=266717;
RA	Walz D.A., Hewett-Elliott D., Seegers W.H.;
RT	"Amino acid sequence of human prothrombin fragments 1 and 2.";
RL	Proc. Natl. Acad. Sci. U.S.A. 74:1969-1972(1977).
RN	[5]
RP	SEQUENCE OF 315-622.
DR	MEDLINE=7207112; PubMed=873923;
RA	Batkowski R.J., Elion J., Downing M.R., Mann K.G.;
RT	"Primary structure of human prethrombin 2 and alpha-thrombin.";
RL	J. Biol. Chem. 252:4942-4957(1977).
RN	[6]
RP	PROCESSING.
DR	MEDLINE=8700532; PubMed=3159958;
RA	Rabiet M.J., Blasini A., Furie B., Furie B.C.;
RT	"Prothrombin fragment 1 X 2 X 3, a major product of prothrombin activation in human plasma.";
RL	J. Biol. Chem. 261:13210-13215(1986).
RN	[7]
RP	X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
DR	MEDLINE=9005942; PubMed=2503108;
RA	Bode W., Mayr T., Baumann U., Huber R., Stone S.R., Hofsteenge J.;
RT	"The refined 1.9 Å crystal structure of human alpha-thrombin: interaction with D-Phe-Pro-Arg chloromethylketone and significance of
RT	interaction with Pro-Pro-Trp insertion segment.";

RL EMBO J. 8:3467-3475(1989).  
 RN [18] RL Biochemistry 28:2078-2082(1989).  
 RP RN  
 RX X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 MEDLINE=90327074; PubMed=237426;  
 Rydel T.J., Ravichandran K.G., Tulinsky A., Bode W., Huber R.,  
 RA Roitch C., Renton J.W. II;  
 RT "The structure of a complex of recombinant hirudin and human alpha-  
 RT thrombin.";  
 RT Science 249:277-280(1990).  
 RN [19] RL  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 MEDLINE=91350942; PubMed=071120;  
 RA Rydel T.J., Yin M., Padmanabhan K.P., Blankenship D.T., Cardin A.D.,  
 RA Correa P.E., Fenton J.W. II, Tulinsky A.;  
 RT "Crystallographic structure of human gamma-thrombin.";  
 RL J. Biol. Chem. 269:22000-22006(1994).  
 RN [10] RL  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).  
 MEDLINE=97357266; PubMed=9214615; DOI=10.1093/embcj/16.11.2977;  
 RA van de Locht A., Bode W., Huber R., Le Bonniec B.F., Stone S.R.,  
 RA Esmon C.T., Stubbs M.T.;  
 RT "The thrombin E192Q-BP1 complex reveals gross structural  
 RT rearrangements: implications for the interaction with antithrombin and  
 RT thrombomodulin.";  
 RL EMBO J. 16:2977-2984(1997).  
 RN [11] RL  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 328-601.  
 RX MEDLINE=99162521; PubMed=10051558; DOI=10.1073/pnas.96.5.1852; Cera E.,  
 RA Guinoto E.R., Caccia S., Rose T., Fuerterer K., Wakeman G., di Cera E.,  
 RT "Unexpected crucial role of residue 314 in serine proteases";  
 PRO. Natl. Acad. Sci. U.S.A. 96:1852-1857(1999).  
 RN [12] RL  
 RP VARIANT DISPROTHROMBINEMA CYS-314.  
 RX MEDLINE=87033739; PubMed=3771562;  
 RA Rabiet M.J., Furie B.C., Furie B.;  
 RT "Molecular defect of prothrombin Barcelona. Substitution of cysteine  
 RT for arginine at residue 273.";  
 J. Biol. Chem. 261:15045-15048(1986).  
 RN [13] RL  
 RP VARIANT DISPROTHROMBINEMA ALA-509.  
 RX MEDLINE=93313001; PubMed=7792330;  
 RA Degen S.J.P., McDowell S.A., Sparks L.M., Scharrer I.;"  
 RT "Prothrombin Frankfurt: a dysfunctional prothrombin characterized by  
 RT substitution of Glu-466 by Ala.";  
 RT Thromb. Haemost. 73:203-209(1995).  
 RN [14] RL  
 RP VARIANT DISPROTHROMBINEMA THR-380 AND HIS-431.  
 RX MEDLINE=9343312; PubMed=1421398;  
 RA Morishita E., Saito M., Kumabashiri I., Asakura H., Matsuda T.,  
 RA Yamaguchi K.;"  
 RT "Prothrombin Himi: a compound heterozygote for two dysfunctional  
 RT prothrombin molecules (Met-337-->Thr and Arg-388-->His).";  
 RT Blood 80:2275-2280(1992).  
 RL [15] RL  
 RP VARIANT DISPROTHROMBINEMA HIS-314.  
 RX MEDLINE=95169838; PubMed=865949;  
 RA James H.L., Kim D.-O., Girolami A.;"  
 RT "Prothrombin Padua I: incomplete activation due to an amino acid  
 RT substitution at a factor Xa cleavage site.";  
 RL Blood Coagul. Fibrinolysis 5:941-944(1994).  
 RN [16] RL  
 RP VARIANT DISPROTHROMBINEMA CYS-425.  
 RX MEDLINE=89207504; PubMed=3242619;  
 RA Henriksen R.A., Mann K.G.;"  
 RT "Identification of the primary structural defect in the dysprothrombin  
 RT thrombin Quick I: substitution of cysteine for arginine-382.";  
 RL Biochemistry 27:9160-9165(1988).  
 RN [17] RL  
 RP VARIANT DISPROTHROMBINEMA VAL-601.  
 RX MEDLINE=89247398; PubMed=271946;  
 RA Henriksen R.A., Mann K.G.;"  
 RT "Substitution of valine for glycine-558 in the congenital dysprothrombin  
 thrombin Quick II alters primary substrate specificity.";  
 RT thrombin Quick II alters primary substrate specificity.";

RL Biochemistry 28:2078-2082(1989).  
 RN [18] RL  
 RP VARIANT DISPROTHROMBINEMA ALA-509.  
 RX MEDLINE=92378975; PubMed=135985;  
 RA Miyata T., Aruga R., Umezawa H., Bezeaud A., Guillen M.-C.,  
 RA Iwanaga S.;"  
 RT "Prothrombin Salakta: substitution of glutamic acid-466 by alanine  
 reduces the fibrinogen clotting activity and the esterase activity.";  
 RL Biochemistry 31:7457-7462(1992).  
 RN [19] RL  
 RP VARIANT DISPROTHROMBINEMA TRB-461.  
 RX MEDLINE=87185407; PubMed=3567158;  
 RA Miyata T., Morita T., Inomoto T., Kawauchi S., Shirakami A.,  
 RA Iwanaga S.;"  
 RT "Prothrombin Tokushima, a replacement of arginine-418 by tryptophan  
 RT that impairs the fibrinogen clotting activity of derived thrombin  
 RL Tokushima.;"  
 RL Biochemistry 26:1117-1122(1987).  
 RN [20] RL  
 RP VARIANT DISPROTHROMBINEMA TRB-461.  
 RX MEDLINE=87101511; PubMed=3801671;  
 RA Inomoto T., Shirakami A., Kawauchi S., Shigekiyo T., Saito S.,  
 RA Miyoshi K., Morita T., Iwanaga S.;"  
 RT "Prothrombin Tokushima: characterization of dysfunctional thrombin  
 RT derived from a variant of human prothrombin.";  
 RL Blood 69:565-569(1987).  
 RN [21] RL  
 RP VARIANT DISPROTHROMBINEMA TRB-461.  
 RX MEDLINE=92256895; PubMed=1349838;  
 RA Iwahana H., Yoshimoto K., Shigekiyo T., Shirakami A., Saito S.,  
 RA Itakura M.;"  
 RT "Detection of a single base substitution of the gene for prothrombin  
 RT Tokushima. The application of PCR-SSCP for the genetic and molecular  
 RT analysis of dysprothrombinemia.";  
 RL Int. J. Hematol. 55:93-100(1992).  
 RN [22] RL  
 RP VARIANT DISPROTHROMBINEMA LYS-200.  
 RX MEDLINE=83204607; PubMed=6405779;  
 RA Board P.G., Shaw D.C.;"  
 RT "Determination of the amino acid substitution in human prothrombin  
 RT type 3 (157 Glu leads to Lys) and the localization of a third thrombin  
 RT cleavage site.";  
 RL Br. J. Haematol. 54:245-254(1983).  
 RN [23] RL  
 RP VARIANT MET-165 AND THR-386.  
 RX MEDLINE=93318093; PubMed=10391209; DOI=10.1038/10290;  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane E.P., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschitz R., Daley G.Q.,  
 RA Lander E.S.;"  
 RT "Characterization of single-nucleotide polymorphisms in coding regions  
 RT of human genes.";  
 RL Nat. Genet. 22:231-238(1999).  
 RN [24] RL  
 RP ERRATUM.  
 RX PubMed=10545957;  
 RA Cargill M., Altschuler D., Ireland J., Sklar P., Ardlie K., Patil N.,  
 RA Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,  
 RA Friedland L., Rolfe A., Warrington J., Lipschitz R., Daley G.Q.,  
 RA Lander E.S.;"  
 RL Nat. Genet. 23:373-373(1999).  
 CC -1- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys'.  
 CC converts fibrinogen to fibrin and activates factors V, VII, VIII, XII, and, in complex with thrombomodulin, protein C.  
 CC -1- CATALYTIC ACTIVITY: Preferential cleavage: Arg-|-Gly; activates  
 CC fibrinogen to fibrin and releases fibrinopeptide A and B.  
 CC -1- SUBCELLULAR LOCATION: Extracellular.  
 CC -1- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.  
 CC -1- PTM: The gamma-carboxylglutamyl residues, which bind calcium ions<sup>B</sup>,  
 CC result from the carboxylation of glutamyl residues by a microsomal

Query Match 100.0%; Score 131, DB 1, Length 622;  
 Best Local Similarity 100.0%; Pred. No. 2.98-09;

Matches	23; Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1 AGYKPDEGKGDAECGDSGGPFV	23						
Db	551 AGYKPDEGKGDAECGDSGGPFV	573						
RESULT 5								
Q27P3	PRELIMINARY;	PRT;	622 AA.					
ID	Q72P3							
AC	Q72P3;							
DT	01-OCT-2003 (TREMBLel. 25, Last sequence update)							
DB	01-MAR-2004 (TREMBLel. 26, Last annotation update)							
OS	Homo sapiens (Human)							
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;							
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;							
NCBI_TAXID	9606;							
[1]								
SEQUENCE FROM N.A.								
RP	TISSUE=Liver;							
RP	MEDLINE=2238827; PubMed=12477932; DOI=10.1073/pnas.242603899;							
RP	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,							
RA	Klauser R.D., Collins F.S., Wagner L., Shemesh C.M., Schuler G.D.,							
RA	Altschul S.F., Zeeberg B., Bustow K.H., Schaefer C.F., Bhat N.K.,							
RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heileh F.,							
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,							
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,							
RA	Brownstein M.J., Usdin T.B., Toshimori S., Chrencik P., Prange C.,							
RA	Raha S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullahy S.J.,							
RA	Richards S., McElroy K.J., McKernan J.A., Gumaratne P.H.,							
RA	Richardson K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,							
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,							
RA	Faherty J., Helton E., Kettman M., Shadron S., Sanchez A.,							
RA	Whiting M., Madan A., Young A.C., Shvchenko A., Rodriguez G.G.,							
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,							
RA	Rodriguez A.C., Grimwood J., Schmitz J., Butterfield Y.S.,							
RA	Krzewinski M.I., Skalska U., Smailz D.E., Schmerch A., Schein J.E.,							
RA	Jones S.J., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human							
RT	and mouse cDNA sequences", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).							
[2]								
SEQUENCE FROM N.A.								
RP	TISSUE=Liver;							
RA	Strainsberg R.; "Substrates (APR-2003) to the EMBL/GenBank/DBJ databases.							
RA	EMBL: BC051332; AAH51332.1; --.							
DR	HSSP: P00734; I-HAG.							
DR	GO; GO:0005576; C:extracellular; IEA.							
DR	GO; GO:0005509; F:calcium ion binding; IEA.							
DR	GO; GO:0008233; F:peptidase activity; IEA.							
DR	GO; GO:0004295; F:trypsin activity; IEA.							
DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.							
DR	InterPro; IPR000001; Kringle.							
DR	InterPro; IPR001254; Peptidase_S1.							
DR	InterPro; IPR0003966; Peptidase_S1A.							
DR	InterPro; IPR009003; Pept_Ser_Cys.							
DR	PF00059; Trypsin; 1.							
DR	PR00722; CHYMOTRYPSIN.							
DR	PRINTS; PR01505; PROTROMBIN.							
DR	SMART; SM00020; TRY_SPC; 1.							
DR	PROSITE; PSS0240; TRYPSIN_DOM; 1.							
DR	PROSITE; PS00134; TRYPSIN_HIS; UNKNOWN_1.							
DR	PROSITE; PS00135; TRYPSIN_SER; 1.							
KW	HYDROLASE; Protease; Serine protease.							
FT	HYDROLASE; Protease; Serine protease.							
SQ	SEQUENCE 235 AA; NON_TER 1							
DR	PF000594; Gla; 1.							
DR	Pfam; PF00051; Kringle; 2.							
DR	PFAM; PF00035; Kringle; 2.							
DR	SMART; SM00069; GLA; 1.							
DR	SMART; SM00130; KR; 2.							
DR	PROSITE; SM00020; TRY_SPC; 1.							
DR	PROSITE; PS00011; GLA; 1.							
DR	PROSITE; PS00021; KRINGLE 1; 2.							
DR	PROSITE; PS50070; KRINGLE 2; 2.							
DR	PROSITE; PS50240; TRYPSIN_DOM; 1.							
DR	PROSITE; PS00114; TRYPSIN_HIS; UNKNOWN_1.							
DR	PROSITE; PS00115; TRYPSIN_SER; 1.							
KW	HYDROLASE; Kringle; Protease; Serine protease.							
RESULT 7								
Qy	1 AGYKPDEGKGDAECGDSGGPFV	23						
Db	165 AGYKPDEGKGDAECGDSGGPFV	187						

DT 01-APR-1990 (Rel. 14, last sequence update)  
 DT 25-OCT-2004 (Rel. 45, last annotation update)

DE prothrombin precursor (EC 3.4.21.5).

GN Name=F7;

OS *Bos taurus* (Bovine);  
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovine; Bos;

OC NCBI\_TaxID=9913;

[1] RN

RP SBQUENCE FROM N.A.

RX MEDLINE=88245190; PubMed=3379642;

RA Irwin D.M.; Robertson K.A.; McGillivray R.T.A.;

RT "Structure and evolution of the bovine prothrombin gene.;"  
 J. Mol. Biol. 200:31-45(1988).

RN

RP SBQUENCE FROM N.A.

RX MEDLINE=84203525; PubMed=6326805;

RA McGillivray R.T.A.; Davie E.W.;

RT "Characterization of bovine prothrombin mRNA and its translation  
 product.;"  
 Biochemistry 23:1626-1634(1984).

[3] RN

RP SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.

RX MEDLINE=8629631; PubMed=3741881;

RA Magnusson S.; Sottrup-Jensen L.; Petersen T.B.; Claeyns H.;

RL (In) Hemker H.C.; Veitkamp J.J. (eds.);  
 Boerhaave symposium on prothrombin and related coagulation factors,  
 PP.25-46., Leiden University Press, Leiden (1975).

[4] RN

RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.

RX MEDLINE=91111686; PubMed=856869;

RA Park C.H.; Tulinsky A.;

RT "Three-dimensional structure of the kringle sequence: structure of  
 prothrombin fragment 1.;"  
 Biochemistry 25:3977-3982(1986).

RT J. Mol. Biol. 220:481-494(1991).

RN [5]

RP X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.

RX MEDLINE=91111686; PubMed=547238;

RA Soriano-Garcia M.; Padmanabhan K.; de Vos A.M.; Tulinsky A.;

RT "The Ca<sup>2+</sup> ion and membrane binding structure of the Gla domain of Ca-  
 prothrombin fragment 1.;"  
 Biochemistry 31:2554-2566(1992).

[7] RN

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RX MEDLINE=92218459; PubMed=1560030;

RA Martin P.D.; Robertson W.; Turk D.; Huber R.; Bode W.; Edwards B.P.P.;

RT "The structure of residues 7-16 of the A alpha-chain of human  
 fibrinogen bound to bovine thrombin at 2.3-A resolution.;"  
 J. Biol. Chem. 267:7911-7920(1992).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RX MEDLINE=92389319; PubMed=1518066;

RA Brandstetter H.; Turk D.; Hoeven H.W.; Grosse D.; Stuerzebecher J.;

RA Martin P.D.; Edwards B.P.P.; Bode W.;

RT "Refined 2.3 A X-ray crystal structure of bovine thrombin complexed  
 formed with the benzamidine and arginine-based thrombin inhibitors  
 NAPAP, 4-TNPAP and WOPA. A starting point for improving  
 antithrombotics;"  
 J. Mol. Biol. 226:1085-1089(1992).

RN [9]

RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.

RX MEDLINE=97102783; PubMed=947033;

RA van de Locht A.; Stubbs M.T.; Bode W.; Friedrich T.; Bollsweiler C.;

RA Hoffken W.; Huber R.;

RT "The ornithodorin-thrombin crystal structure, a key to the TAP  
 enigma?;"

RN

RL EMBO J. 15:6011-6017(1996).

RN [10] X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIABIN.

RX MEDLINE=98004486; PubMed=934225; DOI=10.1073/pnas.94.22.10845;

RA Fuentess-Prior P.; Noeske-Jungblut C.; Donner P.; Schleuning W.D.;

RA Huber R.; Bode W.

RT "Structure of the thrombin complex with triabin, a lipocalin-like  
 exosite-binding inhibitor derived from a triatomine bug.;"  
 Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).

[11] RN

RP GENE STRUCTURE.

RX MEDLINE=8607773; PubMed=3000440;

RA Irwin D.M.; Ahearn K.G.; Pearson G.D.; McGillivray R.T.A.;

RT "Characterization of the bovine prothrombin gene.;"  
 Biochemistry 24:6854-6861(1985).

CC -I- FUNCTION: Thrombin, which cleaves bonds after Arg and Lys', converts fibrinogen to fibrin and activates factors V, VII, VIII, XIII, and, in complex with thrombinogen, protein C.

CC -I- CATALYTIC ACTIVITY: Preferential cleavage: Arg-1-Gly; activatees fibrinogen to fibrin and releases fibrinopeptide A and B.

CC -I- SUBCELLULAR LOCATION: Extracellular.

CC -I- TISSUE SPECIFICITY: Expressed by the liver and secreted in plasma.

CC -I- PIM: The gamma-carboxyglutamyl residues, which bind calcium ions, result from the carboxylation of glutamyl residues by a microsomal enzyme, the vitamin K-dependent carboxylase. The modified residues are necessary for the calcium-dependent interaction with a negatively charged phospholipid surface, which is essential for the conversion of prothrombin to thrombin.

CC -I- MISCELLANEOUS: Prothrombin is activated on the surface of a phospholipid membrane that binds the amino end of prothrombin and factors Va and Xa in Ca-dependent interactions; factor Xa removes the activation peptide and cleaves the remaining part into light and heavy chains. The activation process starts slowly because factor V itself has to be activated by the initial, small amounts of thrombin.

CC -I- MISCELLANEOUS: Thrombin can itself cleave the amino terminal fragment (fragment 1) of the prothrombin, prior to its activation by factor Xa.

CC -I- SIMILARITY: Belongs to the peptidase S1 family.

CC -I- SIMILARITY: Contains 1 gamma-carboxy-glutamate domain (Gla) domain.

CC -I- SIMILARITY: Contains 2 kringle domains.

CC -I- DATABASE: NAME=Prozyme technical fact sheet;  
 WWW="http://www.prozyme.com/technical/thrombindata.html".

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CC EMBL: V00135; CA2451.1; -.

DR EMBL: J00041; AA30781.1; -.

DR PIR: S02537; TBL0.

DR PDB: 1A0H; X-ray; AD=208-366, B=367-625.

DR PDB: 1AVG; X-ray; H=367-625, L=326-366.

DR PDB: 1BBR; X-ray; E=517-625, H=367-516, J/L/M=318-366, K/N=367-625.

DR PDB: 1ETR; X-ray; H=367-625, L=310-366.

DR PDB: 1ETS; X-ray; H=367-625, L=310-366.

DR PDB: 1ETT; X-ray; H=367-625, L=310-366.

DR PDB: 1HRT; X-ray; H=367-625, L=310-366.

DR PDB: 1ID5; X-ray; H=367-622, L=310-366.

DR PDB: 1MKW; X-ray; H/K/L=.

DR PDB: 1NL2; X-ray; A=4-189.

DR PDB: 1TBQ; X-ray; H/K=367-625, J/L=318-366.

DR PDB: 1TBR; X-ray; H/K=367-625, J/L=318-366.

DR PDB: 1TOC; X-ray; A/C/E/G=310-366, B/D/F/H=367-625.

DR PDB: 1UCY; X-ray; E=517-625, H=367-516, J/L/M=318-366, K/N=367-625.

DR PDB: 1UVU; X-ray; H=367-625, L=310-366.









RN [2]  
 RP  
 RC  
 TISSUE=Liver;  
 RX  
 MEDLINE=2224112; PubMed=12454917; DOI=10.1002/xdy.10174;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 Richardson P.;  
 RT "Genetic and genomic tools for *Xenopus* research: The NIH *Xenopus*  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [3]  
 RP  
 RC  
 TISSUE=Liver;  
 RA Klein S., Gerhard D.S.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073504; AAH73504.1;  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005509; P:calcium ion binding; IEA.  
 DR GO; GO:0004263; P:chymotrypsin activity; IEA.  
 DR GO; GO:0008233; P:peptidase activity; IEA.  
 DR GO; GO:0003805; P:thrombin activity; IEA.  
 DR GO; GO:0004235; P:trypsin activity; IEA.  
 DR GO; GO:0007596; P:blood coagulation; IEA.  
 DR InterPro; IPR002303; GLA\_blood.  
 DR InterPro; IPR000001; Kringle.  
 DR InterPro; IPR00254; Peptidase\_S1.  
 DR InterPro; IPR001314; Peptidase\_SIA.  
 DR InterPro; IPR003966; Peptidase\_SIA\_pr.  
 DR InterPro; IPR005003; Pept\_Ser\_Cys.  
 DR InterPro; IPR000294; VitK\_dep\_GLA.  
 DR Pfam; PF00051; Kringle; 2.  
 DR Pfam; PF00089; Trypsin; 1.  
 DR Prints; PR00722; CHYMOTRYPSIN.  
 DR Prints; PR00001; GLABLOOD.  
 DR Prints; PR00118; KRINGLE.  
 DR Prints; PR01505; PROTHROMBIN.  
 DR ProDom; PD000335; PROTHROMBIN.  
 DR SMART; SM00069; GLA; 1.  
 DR SMART; SM00130; KR; 2.  
 DR SMART; SM00020; TRYSPC; 1.  
 DR PROSITE; PS50021; KRINGLE\_1; 2.  
 DR PROSITE; PS50070; KRINGLE\_2; 2.  
 DR PROSITE; PS50240; TRYPSIN\_DON; 1.  
 DR PROSITE; PS00134; TRYPSIN\_HIS; UNKNOWN\_1.  
 DR PROSITE; PS00135; TRYPSIN\_SER; 1.  
 KW Hydrolase, Kringle, Protease, Serine protease.  
 FT  
 NON\_TER 1  
 SEQUENCE 615 AA; 70195 MW; 9063E80059336E1 CRC64;  
 Query Match 86.3%; Score 113; DB 2; Length 615;  
 Best Local Similarity 82.6%; Pred. No. 7\_7e-07;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 AGYKPEDEGERGDAEGDGGPFV  
 Db 543 AGYKPEDEGERGDAEGDGGPFV 565

Search completed: March 31, 2005, 01:55:59

Job time : 185 secs

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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on:

March 31, 2005, 01:46:47 ;

Search time 43 Seconds

(without alignments)

51.465 Million cell updates/sec

Title: US-10-766-752B-5  
 Perfect score: 131  
 Sequence: 1 AGYKPKPDESKRGDACEGDSGGPFV 23

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

PIR 79,\*

1: pir1;\*

2: pir2;\*

3: pir3;\*

4: pir4;\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

% Query Match Length DB ID

Description

1	131	100.0	622	1	TRHU	thrombin (EC 3.4.21.5) precursor [validated] - human
2	127	96.9	236	2	C42696	N/Contains: prothrombin
3	124	94.7	625	1	TBBO	C-Species: Homo sapiens (man)
4	118	90.1	234	2	P42696	C;Accession: A39351; A00914; B00914; A37549; A37550; 151952
5	113	86.3	235	2	DA2696	R;Degen, S.J.P.; Davie, E.W.
6	110	84.0	236	2	E42696	Biochemistry 26, 615-617, 1987
7	109	83.2	239	2	G42696	A;Title: Nucleotide sequence of the gene for human prothrombin.
8	102	77.9	617	2	S0511	A;Reference number: A29351; MUID:8807877; PMID:2825773
9	102	77.9	618	1	A5827	A;Accession: A29351
10	89	67.9	235	2	H42696	A;Molecule type: DNA
11	71.5	54.6	417	1	S00845	A;Cross-references: UNIPROT:PO0734; GB: M17262; GB: M33691; NID: 9558069; PIDN: AAC3054.1; R;Degen, S.J.P.; MacGillivray, R.T.A.; Davie, E.W.
12	71	54.2	461	1	KXHU	A;Molecule type: DNA
13	70.5	53.8	482	1	EXRT	A;Residues: 1-622 <DB3>
14	70.5	53.8	638	1	QKRP	A;Cross-references: GB:V00595; GB:J00307; NID:937128; PIDN:CAA23842.1; PID:91335344
15	69.5	53.1	275	2	S4007	A;Accession: B00914
16	69.5	53.1	1524	2	T30337	A;Molecule type: mRNA
17	69.5	53.1	161	2	16244	A;Residues: 8-163, 'N', 165-622 <DE2>
18	68.5	52.3	461	1	EXRT	A;Accession: B00914
19	68.5	52.3	488	1	EXRU	A;Molecule type: DNA
20	68.5	52.3	1019	2	A39350	A;Reference number: A37551; MUID:87008532; PMID:3759958
21	67.5	51.5	161	2	I44158	A;Contents: annotation ; activation cleavages
22	67.5	51.5	282	2	I44621	A;Accession: A37550
23	67.5	51.5	459	2	JO0419	A;Molecule type: protein
24	67.5	51.5	475	1	EXCH	A;Residues: 315-334, 'N', 336-348, 'N', 350-368, 'N', 370-397, 'N', 399-413, 'N', 415-484, 'N', 486-
25	67.5	51.5	638	1	KQNSPL	R;Rabiet, M.J.; Blahnik, A.; Furie, B.; Furie, B.C.
25	67	51.1	225	2	S45356	J. Biol. Chem. 261: 13210-13215, 1986
27	67	51.1	264	2	S32794	A;Reference number: A37552; MUID:87182874; PMID:3471151
28	66.5	50.8	309	2	BR9878	A;Status: translated from GB/EMBL/DBJ
29	66.5	50.8	1004	2	T30338	A;Molecule type: mRNA

#### ALIGNMENTS

trypsin (EC 3.4.21.1)  
 trypsin (EC 3.4.21.2)  
 trypsin (EC 3.4.21.3)  
 trypsin (EC 3.4.21.4)  
 plasma kallikrein  
 serine protease  
 trypsin-like prote  
 complement factor  
 complement factor  
 protein C (activat  
 nucleol protein prec  
 coagulation factor  
 protein C (activat  
 limulus clotting e  
 hepsin (EC 3.4.21.  
 coagulation factor

30	65.5	50.0	267	2	S40006	trypsin (EC 3.4.21.1)
31	65.5	50.0	274	2	S35339	trypsin (EC 3.4.21.2)
32	65.5	50.0	275	2	S35340	trypsin (EC 3.4.21.3)
33	65.5	50.0	277	2	S35340	trypsin (EC 3.4.21.4)
34	65.5	50.0	638	1	KQRTPL	plasma kallikrein
35	64.5	49.2	237	2	S55378	serine protease
36	64.5	49.2	238	1	TRWVSY	trypsin-like prote
37	64	48.9	191	2	SS4115	complement factor
38	64	48.9	246	1	DBHU	complement factor
39	64	48.9	456	1	KXBO	protein C (activat
40	64	48.9	2616	1	A57096	nucleol protein prec
41	63.5	48.5	625	1	KFHU1	coagulation factor
42	63	48.1	461	1	JX2010	protein C (activat
43	62.5	47.7	375	1	A23689	limulus clotting e
44	62.5	47.7	416	1	S3377	hepsin (EC 3.4.21.
45	62.5	47.7	492	1	EXBO	coagulation factor

A;Residues: 1-2, 'RI', 5-100 <REBS>

A;Cross-references: GB:W3031; NID:9190723; PID:AA60220.1; PID:9190724  
 C;Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fibrin  
 C;Comment: Prothrombin is activated on the surface of a phospholipid membrane that binds  
 C; can be removed either by factor Xa or thrombin; the cleavage into light and heavy chain  
 ter 314-Arg, are released in natural blood clotting.  
 C;Comment: The cleavage after Arg198, observed *in vitro*, does not occur in plasma.  
 C;Comment: The gamma-carboxyglutamyl residues bind calcium ions, result from the carboxy-  
 ent interaction with the negatively charged phospholipid membrane surface.  
 C;Genetics:  
 A;Gene: GDB:F2  
 A;Cross-references: GDB:119894; OMIM:176930  
 A;Map position: 11p11-11q12  
 A;Introns: 27/1; 80/3; 85/1; 106/1; 141/2; 187/1; 292/1; 335/1; 377/2; 433/2; 491/2; 552  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: acute phase; blood coagulation; calcium binding; carboxyglutamic acid; dupli-  
 F;1-24/Domain: signal sequence #status predicted <SIG>  
 F;1-25-43/Domain: propeptide #status predicted <PRO>  
 F;2-87/Domain: Gla domain homology <GLA>  
 F;44-62/Domain: prothrombin #status experimental <MPT>  
 F;45-327/Domain: activation peptide #status experimental <APT>  
 F;0-8-186/Domain: kringle homology <KR1>  
 F;213-291/Domain: kringle homology <KR2>  
 F;28-363/Domain: propeptide #status predicted <PRO>  
 F;364-622/Domain: thrombin heavy chain #status experimental <UCH>  
 F;49-50-57-59-62-63-68-69-72-75/Domain: Modified site: gamma-carboxyglutamic acid (glu) #status  
 F;60-65-90-103-108-186-129-169-157-181-213-291-234-74-262-286/Diulfide bonds: #status  
 F;122-143/Domain: carbonylate (Asn) (covalent) #status predicted  
 F;336-412-536-550-564-594/Diulfide bonds: #status predicted  
 F;391-407/Active site: His, Asp #status predicted  
 F;416/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F;568/active site: Ser #status experimental

Query Match 100.0% Score 131; DB 1; Length 622;  
 Best Local Similarity 100.0%; Pred. No. 2e-10;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGEGKDACEGDSGGPFV 23  
 DB 551 AGYKPDGEGKDACEGDSGGPFV 573

RESULT 2

C42696 thrombin (EC 3.4.21.5) B chain - rabbit (fragment)  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Accession: C42696  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: C42696  
 C;Bankfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq-  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Accession: C42696  
 A;Status: Preliminary; nucleic acid sequence not shown; not compared with conceptual tra-  
 A;Molecule type: mRNA  
 A;Residues: 1-236 <BAN>  
 A;Cross-references: UNIPROT:Q28731; GB:W91396  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-227/Domain: trypsin homology (fragment) <TRY>  
 Query Match 96.9% Score 127; DB 2; Length 236;  
 Best Local Similarity 95.7%; Pred. No. 2.8e-10; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPDGEGKDACEGDSGGPFV 23  
 DB 165 AGYKPDGEGKDACEGDSGGPFV 187

RESULT 3

F;200-317/Domain: activation peptide 2 #status experimental <FR2>  
 F;218-292/Domain: kringle homology <KR2>  
 F;310-366/Product: thrombin light chain #status experimental <LC1>  
 F;367-625/Product: thrombin heavy chain #status experimental <HC1>  
 F;50, 51, 59, 60, 63, 64-69, 73, 76/Modified site: gamma-carboxyglutamic acid (Glu) #status experimental  
 F;61-66, 91-104, 109-187, 180-170, 158-182, 214-222, 235-275, 263-287, 339-485, 394-410, 539-553, 5  
 F;120, 144-419/Binding site: carbohydrate (Abn) (covalent) #status experimental  
 F;403, 465, 571/Active site: His, Asp, Ser #status experimental

Query Match 94.7%; Score 124; DB 1; Length 625;  
 Best Local Similarity 95.7%; Pred. No. 1.8e-09; 1; Indels 0; Gaps 0;  
 Matches 22; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGDAECDSGGPFV 23  
 Db 554 AGYKPKGKRGDAECDSGGPFV 576

RESULT 4

thrombin (EC 3.4.21.5) B chain - *Cynops pyrocastor* (fire-bellied newt) (fragment)  
 C;Species: *Cynops pyrocastor* (fire-bellied newt)  
 C;Date: 19-Mar-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
 C;Accession: F42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Note: sequence not  
 A;Accession: F42696  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Molecule type: mRNA  
 A;Residues: 1-334 <BAN>  
 C;Cross-references: UNIPROT:Q90387; GB:W81395  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase

Query Match 90.1%; Score 118; DB 2; Length 234;  
 Best Local Similarity 91.3%; Pred. No. 4.9e-09; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGDAECDSGGPFV 23  
 Db 163 AGYKPKDEGKRGDAECDSGGPFV 185

RESULT 5

D42696 thrombin (EC 3.4.21.5) B chain - chicken (fragment)  
 C;Species: *Gallus gallus* (chicken)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: D42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-236 <BAN>  
 C;Cross-references: UNIPROT:Q90504; GB:W81393  
 A;Note: nucleotide translation not given  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 84.0%; Score 110; DB 2; Length 236;  
 Best Local Similarity 82.6%; Pred. No. 6.3e-08; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGDAECDSGGPFV 23  
 Db 164 AGYSPEDMKRGDAECDSGGPFV 186

RESULT 6

D42696 thrombin (EC 3.4.21.5) B chain - *tokay* (fragment)  
 C;Species: *Gekko gecko* (tokay)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: D42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra  
 A;Accession: D42696  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <BAN>  
 A;Cross-references: UNIPROT:Q91004; GB:W81392  
 A;Note: sequence not  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 86.3%; Score 113; DB 2; Length 235;  
 Best Local Similarity 82.6%; Pred. No. 2.4e-08; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGDAECDSGGPFV 23  
 Db 164 AGYSPEDMKRGDAECDSGGPFV 186

RESULT 7

D42696 thrombin (EC 3.4.21.5) B chain - *Pacific hagfish* (fragment)  
 C;Species: *Eptatretus stouti* (Pacific hagfish)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: I42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Accession: I42696  
 A;Status: preliminary; not compared with conceptual translation  
 A;Molecule type: mRNA  
 A;Residues: 1-236 <BAN>  
 C;Cross-references: UNIPROT:Q90504; GB:W81393  
 A;Note: nucleotide translation not given  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: hydrolase; serine proteinase  
 F;1-226/Domain: trypsin homology (fragment) <TRY>

Query Match 84.0%; Score 110; DB 2; Length 236;  
 Best Local Similarity 82.6%; Pred. No. 6.3e-08; 2; Mismatches 0; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AGYKPKDEGKRGDAECDSGGPFV 23  
 Db 164 AGYSPEDMKRGDAECDSGGPFV 186

RESULT 8

D42696 thrombin (EC 3.4.21.5) B chain - rainbow trout (fragment)  
 C;Species: *Oncorhynchus mykiss* (rainbow trout)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: G42696

R;Banfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and seq  
 A;Reference number: G42696; MUID:92212913; PMID:1557383  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-239 <BAN>

Query Match      83.2%; Score 109; DB 2; Length 239;  
 Best Local Similarity 82.6%; Pred. No. 8.8e-08; DB 2; Mismatches 2; Indels 0; Gaps 0;  
 Matches 19; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 9  
 S10511

thrombin (EC 3.4.21.5) precursor - rat  
 C;Species: *Rattus norvegicus* (Norway rat)  
 C;Date: 07-May-1993 #sequence\_revision 07-May-1993 #text\_change 09-Jul-2004  
 R;Dihanchik, M.; Monard, D.  
 Nucleic Acids Res. 18, 4251, 1990  
 A;Title: cDNA sequence of rat prothrombin.  
 A;Reference number: S10511; MUID:9033426; PMID:2377469  
 A;Accession: S10511  
 A;Molecule type: mRNA  
 A;Residues: 1-617 <DIN>  
 A;Cross-references: UNIPROT:P18292; EMBL:X52835; NID:956969; PID:CAA37017.1; PID:956970  
 R;Henrikson, K.P.; Jazin, E.E.; Greenwood, J.A.; Dickerman, H.W.  
 Endocrinology/126, 167-175, 1990  
 A;Title: Prothrombin levels are increased in the estrogen-treated immature rat uterus.  
 A;Reference number: A60576; MUID:90091942; PMID:2293980  
 A;Accession: A60576  
 A;Molecule type: protein  
 A;Residues: 44-58 <HEN>  
 A;Note: the authors purified the proenzyme from the estrogen-stimulated maturing rat uterus.  
 R;Bainfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing.  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Accession: B42696  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 383-617; E' <BAN>  
 A;Cross-references: GB:MB1397  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 C;Keywords: blood coagulation; calcium binding; carboxyglutamic acid; glycoprotein; hydrolytic enzymes  
 F;1-24/Domain: signal sequence #status Predicted <SIG>  
 F;25-43/Domain: propertide #status Predicted <PRO>  
 F;44-68/Domain: Gla domain homology <GLA>  
 F;44-68/Domain: Gla domain homology <GLA>  
 F;44-68/Domain: prothrombin #status experimental <PMAT>  
 F;109-187/Domain: kringle homology <KR1>  
 F;215-292/Domain: kringle homology <KR2>  
 F;361-610/Domain: trypsin homology <TRY>  
 F;61-66, 91-104, 109-187, 130-170, 158-182, 215-293, 236-276, 261-288, 333-479, 388-404, 533-547, 548-556/Domain: prothrombin B #status Predicted <PRO>  
 F;403, 459, 565/Active site: His, ASP, Ser #status Predicted <PRO>  
 Query Match      77.9%; Score 102; DB 2; Length 618;  
 Best Local Similarity 78.3%; Pred. No. 2e-06; DB 2; Mismatches 3; Indels 0; Gaps 0;  
 Matches 18; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 11  
 H42696

thrombin (EC 3.4.21.5) B chain - white sturgeon (fragment)  
 C;Species: *Acipenser transmontanus* (white sturgeon)  
 C;Date: 26-May-1994 #sequence\_revision 26-May-1994 #text\_change 09-Jul-2004  
 C;Accession: H42696  
 R;Bainfield, D.K.; MacGillivray, R.T.A.  
 Proc. Natl. Acad. Sci. U.S.A. 89, 2779-2783, 1992  
 A;Title: Partial characterization of vertebrate prothrombin cDNAs: amplification and sequencing.  
 A;Reference number: A42696; MUID:92212913; PMID:1557383  
 A;Accession: H42696  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-235 <BAN>  
 A;Cross-references: UNIPROT:Q90244; GB:MB1399  
 C;Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology  
 F;1-226/Domain: trypsin homology (fragment) <TRY>  
 Query Match      67.9%; Score 89; DB 2; Length 235;  
 Best Local Similarity 65.2%; Pred. No. 5.1e-05; DB 2; Mismatches 5; Indels 0; Gaps 0;  
 Matches 15; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

RESULT 10  
 A35827

thrombin (EC 3.4.21.5) precursor - mouse  
 C;Species: *Mus musculus* (house mouse)  
 C;Date: 14-Dec-1990 #sequence\_revision 14-Dec-1990 #text\_change 09-Jul-2004  
 C;Accession: A35827; A42296; S12081

Query Match      1 AGYKPDEGKGDAEGDGGPFV 23  
 Best Local Similarity 65.2%; Pred. No. 5.1e-05; DB 2; Mismatches 5; Indels 0; Gaps 0;

Db      547 AGFKVNDTKRGDAEGDGGPFV 569

Query Match      1 AGYKPDEGKGDAEGDGGPFV 23  
 Best Local Similarity 65.2%; Pred. No. 5.1e-05; DB 2; Mismatches 5; Indels 0; Gaps 0;

Db      164 AGFSPEDESDTSGSACEGDGGPFV 186

RESULT 12  
 S00845  
 heparin (EC 3.4.21.-) - human



J. Biochem. 103, 890-898, 1991  
 A;Title: Characterization of rat factors X and Xa: demonstration of factor Xa in rat pla  
 A;Reference number: PS0190; MUID:92041742; PMID:1718949  
 A;Accession: PS0191  
 A;Molecule type: protein  
 A;Residues: 41-58, 'X', 60-65 <EN1>  
 A;Accession: PS0190  
 A;Molecule type: protein  
 A;Residues: 183-186, 'X', 188-207 <EN2>  
 A;Reference number: I46196; MUID:9422160; PMID:8168595  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 295-383, G', 385-455 <MUR>  
 A;Cross-references: GB:D21215; NID:9415309; PIDN:BA04756.1; PID:9455396  
 C;Function:  
 A;Description: catalyzes the proteolytic activation of prothrombin to thrombin in the pr  
 A;Pathway: blood coagulation  
 C;Superfamily: coagulation factor X; EGF homology; Gla domain homology; trypsin homology  
 C;Keywords: beta-hydroxyaspartic acid; blood coagulation; calcium binding; carboxyglutam  
 F:1-23/Domain: signal sequence #status predicted <SG>  
 F:1-24/Domain: propenote #status predicted <PRO>  
 F:1-25/Domain: Gla domain homology <GLA>  
 F:41-179/Domain: coagulation Factor X light chain #status predicted <LCH>  
 F:90-121/Domain: EGF homology <EG1>  
 F:129-164/Domain: EGF homology <EG2>  
 F:183-482/Product: coagulation factor X heavy chain #status predicted <HCH>  
 F:184-231/Domain: activation peptide #status predicted <APT>  
 F:232-482/Product: coagulation factor Xa heavy chain #status predicted <ACT>  
 F:232-460/Domain: trypsin homology <TRY>  
 F:232-460/Domain: trypsin homology <TRY>  
 F:46-47, 54-56, 59-60, 65-66, 72-79/Modified site: gamma-carboxyglutamic acid (Glu) #statu  
 F:57-62, 90-101, 95-110, 112-121, 129-140, 136-149, 151-164, 172-200, 238-243, 259-275, 388-402, 41  
 F:103/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status predicted  
 F:107/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:208/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:218/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:231-232/Cleavage site: Arg-Asp (coagulation factor Xa, coagulation factor Vira) #statu  
 F:274, 320, 417/Active site: His, Asp, Ser #status predicted  
 Query Match 53.8%; Score 70.5; DB 1; Length 482;  
 Best local Similarity 60.9%; Pred. No. 0.037;  
 Matches 14; Conservative 3; Mismatches 3; Indels 3; Gaps 1;  
 Qy 1 AGYKPDDEGKGDAEFGDGGPFV 23  
 Db 403 AGY--DAKQEDACOGDGGPHV 422

RESULT 15

KOHPII  
 plasma kallikrein (EC 3.4.21.34) precursor - human  
 N;Alternate names: kininogenin; plasma prekallikrein  
 C;Species: Homo sapiens (man)  
 C;Date: 13-Aug-1986 #sequence\_change 09-Jul-2004  
 C;Accession: A00921; A37939  
 R;Chung, D.W.; Fujikawa, K.; McMullen, B.A.; Davie, E.W.  
 B;Biochemistry 25, 2410-2417, 1986  
 A;Title: Human plasma prekallikrein, a zymogen to a serine protease that contains four t  
 A;Reference number: A00921; MUID:86243359; PMID:3521732  
 A;Accession: A00921  
 A;Molecule type: mRNA  
 A;Residues: 1-638 <CHU>  
 A;Cross-references: UNIPROT:PO3952; GB:MI3143; NID:9190262; PIDN:AA60153.1; PID:9190263  
 R;McMullen, B.A.; Fujikawa, K.; Davie, E.W.  
 Biochemistry 30, 2050-2056, 1991  
 A;Title: Location of the disulfide bonds in human plasma prekallikrein: the presence of  
 A;Reference number: A37939; MUID:91152016; PMID:199866  
 A;Accession: A37939  
 A;Molecule type: protein  
 A;Residues: 20-27;40-46, 'X', 48, 'H', 50, 'X', 52-70, 'H'; 75-76, 'X', 78-80;103-113;131-140;141-

; 260-283, 'X', 285-287-291, 'X', 293-295;314-317, 'X', 319-320;321-324, 'X', 329-333;334-339, 'X'  
 525;533-551;562, 'X', 564-567-573, 'X', 575-576;578-583, 'X', 585;592-604 <MCN>  
 C;Comment: This protein, synthesized in the liver, circulates as a noncovalent complex w  
 C;are linked by one or more disulfide bonds.  
 C;Comment: The enzyme cleaves Lys-Arg and Arg-Ser bonds. It activates, in a reciprocal r  
 inogen and may also play a role in the renin-angiotensin system by converting prorenin i  
 C;Genetics:  
 A;Gene: GDB:KLK3  
 A;Map position: 4q35-4q35  
 A;Superfamily: coagulation factor XI; trypsin homology  
 C;Keywords: blood coagulation; duplication; fibrinolysis; glycoprotein; hydrolase; infla  
 F:1-19/Domain: signal sequence #status predicted <SG>  
 F:20-638/Domain: plasma kallikrein #status predicted <MMT>  
 F:20-390/Domain: plasma kallikrein heavy chain #status predicted <HCH>  
 F:20-109/Domain: apple repeat <API>  
 F:10-199/Domain: apple repeat <AP2>  
 F:200-289/Domain: apple repeat <AP3>  
 F:291-380/Domain: apple repeat <AP4>  
 F:391-638/Domain: plasma kallikrein light chain #status predicted <LCH>  
 F:391-621/Domain: trypsin homology <TRY>  
 F:21-104, 47-77, 51-57, 111-194, 137-166, 41-147, 201-284, 227-256, 231-237, 292-375, 322-328, 383  
 F:127, 308, 396, 453, 494/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F:318-347, 349-345/disulfide bonds: #status predicted  
 F:3390-391/Cleavage site: Arg-Lys (coagulation factor XIIa) #status predicted  
 F:434, 483, 578/Active site: His, Asp, Ser #status predicted

Query Match 53.8%; Score 70.5; DB 1; Length 638;  
 Best Local Similarity 69.6%; Pred. No. 0.049;  
 Matches 16; Conservative 2; Mismatches 2; Indels 3; Gaps 2;  
 Qy 1 AGYKPDDEGKGDAEFGDGGPFV 23  
 Db 564 AGYK--DAKQEDACOGDGGPHV 583

Search completed: March 31, 2005, 01:56:47  
 Job time : 44 secs

RESULT 2  
US-08-100-594-8  
Sequence 8, Application US/08330594C  
PATENT NO. 6184342  
GENERAL INFORMATION:  
APPLICANT: CAREY, DARRELL H.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS  
FILE REFERENCE: CBP:002  
CURRENT APPLICATION NUMBER: US/08/330,594C  
CURRENT FILING DATE: 1994-10-28  
NUMBER OF SEQ ID NOS: 9  
SEQ ID NO: 8  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-08-330-594-8

RESULT 3  
US-09-644-038-8  
Sequence 8, Application US/09644038  
PATENT NO. 6603978  
GENERAL INFORMATION:  
APPLICANT: CAREY, DARRELL H.  
TITLE OF INVENTION: SYNTHETIC PEPTIDE NEUTROPHIL CELL CHEMOTACTIC AGENTS  
FILE REFERENCE: CBP:002  
CURRENT APPLICATION NUMBER: US/09/644, 038  
CURRENT FILING DATE: 2000-08-22  
PRIORITY APPLICATION NUMBER: 08/730, 594  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 8  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: Peptide  
US-09-644-038-8

Query Match 100.0%; Score 131; DB 3; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGGRGDACEGDSGGFPV 23  
Db 1 AGYKPKDEGGRGDACEGDSGGFPV 23

RESULT 4  
US-08-538-504-3  
Sequence 8, Application US/08538504  
PATENT NO. 6627731  
GENERAL INFORMATION:  
APPLICANT: Carney, Darrell H.  
TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES:

Query Match 100.0%; Score 131; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGGRGDACEGDSGGFPV 23  
Db 1 AGYKPKDEGGRGDACEGDSGGFPV 23

RESULT 4  
US-08-538-504-3  
Sequence 3, Application US/08538504  
PATENT NO. 6627731  
GENERAL INFORMATION:  
APPLICANT: Glenn, Kevin C.  
TITLE OF INVENTION: THROMBIN DERIVED POLYPEPTIDES:

Query Match 100.0%; Score 131; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGGRGDACEGDSGGFPV 23  
Db 1 AGYKPKDEGGRGDACEGDSGGFPV 23

RESULT 5  
US-09-909-348A-5  
Sequence 5, Application US/09909348A  
PATENT NO. 6815416  
GENERAL INFORMATION:  
APPLICANT: CAREY, DARRELL H.  
APPLICANT: CROWDER, ROGER S.  
APPLICANT: STIERBERG, JANET  
APPLICANT: BERGMANN, JOHN  
TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR  
FILE REFERENCE: 3033.1003-001  
CURRENT APPLICATION NUMBER: US/09/909, 348A  
CURRENT FILING DATE: 2001-07-19  
PRIORITY APPLICATION NUMBER: 60/219, 800  
PRIORITY FILING DATE: 2000-07-20  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FASTSEQ FOR Windows Version 4.0  
SEQ ID NO: 5  
LENGTH: 23  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Peptide fragment of thrombin  
US-09-909-348A-5

Query Match 100.0%; Score 131; DB 4; Length 23;  
Best Local Similarity 100.0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGGRGDACEGDSGGFPV 23  
Db 1 AGYKPKDEGGRGDACEGDSGGFPV 23



TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FEATURE:  
NAME/KEY: Region  
LOCATION: 1..320  
OTHER INFORMATION: /note= "Prothrombin Light Chain"  
FEATURE:  
NAME/KEY: Region  
LOCATION: 321..579  
OTHER INFORMATION: /note= "Prothrombin Heavy Chain"  
US-00-295-411-4

Query Match 100.0%; Score 131; DB 1; Length 579;  
Best Local Similarity 100.0%; Pred. No. 1.2e-10;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 AGYKPPDKRQDACEGDSGGPRV 23  
Db 508 AGYKPPDKRQDACEGDSGGPRV 530

Search completed: March 31, 2005, 01:57:36  
Job time : 44 secs

RESULT 13

US-08-558-269-10

Sequence 10, Application US/08558269

Patent No. 5,961,973

GENERAL INFORMATION:

APPLICANT: Crea, Roberto

TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: ASCII (text)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/558, 269

FILING DATE: 13-NOV-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/847, 800

FILING DATE: 06-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Vincent, Matthew P.

REGISTRATION NUMBER: 36,709

REFERENCE/DOCKET NUMBER: CRI-001CP2

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 376 amino acids

TYPE: amino acid

TOPOLogy: linear

MOLECULE TYPE: protein

US-09-410-882-10

Query Match 100.0% Score 131; DB 2; Length 376; Best Local Similarity 100.0%; Pred. No. 7.5e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDDEKRGDACEGSGGPV 23

Db 305 AGYKPDDEKRGDACEGSGGPV 327

RESULT 14

US-09-410-882-10

Sequence 4, Application US/09410882

Patent No. 6,287,561

GENERAL INFORMATION:

APPLICANT: Crea, Roberto

TITLE OF INVENTION: PATHOGEN-TARGETED BIOCATALYSTS

NUMBER OF SEQUENCES: 26

CORRESPONDENCE ADDRESS:

ADDRESSEE: LAHIVE & COCKFIELD

STREET: 60 State Street

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/295, 411

FILING DATE: 22-AUG-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/793, 989

FILING DATE: 18-NOV-1991

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Fitting, Thomas

REGISTRATION NUMBER: 34,163

REFERENCE/DOCKET NUMBER: TSR1263.001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-554-2937

TELEFAX: 619-554-6312

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 579 amino acids

CURRENT FILING DATE: 2002-06-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: PatentIn version 3.0

SEQ ID NO: 4

LENGTH: 259

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: CHAIN

NAME/KEY: (1)..  
(259)

OTHER INFORMATION: Thrombin WE B-Chain

US-10-165-442-4

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGGPFV 23

Db 188 AGYKPDGKRGDACEGDSGGPFV 210

RESULT 10

US-0-338-368-2

Sequence 2, Application US/08338368

PATENT NO. 6110721

GENERAL INFORMATION:

APPLICANT: GIBBS, CRAIG S.

APPLICANT: LEUNG, LAWRENCE L.K.

APPLICANT: TSUANG, MANUEL

TITLE OF INVENTION: NOVEL POLYPEPTIDES AND COAGULATION

TITLE OF INVENTION: THERAPY

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: GILREAD SCIENCES, INC.

STREET: 353 LAKESIDE DRIVE

CITY: FOSTER CITY

STATE: CALIFORNIA

COUNTRY: USA

ZIP: 94404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/338,368

FILING DATE: 14-NOV-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/258,038

FILING DATE: 10-JUN-1994

ATTORNEY/AGENT INFORMATION:

NAME: HENSLEY, MAX D.

REGISTRATION NUMBER: 27,043

REFERENCE/DOCKET NUMBER: 190-2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-574-3000

TELEFAX: 415-573-4699

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 295 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULAR TYPE: protein

US-0-338-368-2

Query Match 100.0%; Score 131; DB 3; Length 295; Best Local Similarity 100.0%; Pred. No. 5.8e-11; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11

US-10-165-442-1

Sequence 1, Application US/10165442

PATENT NO. 6706512

GENERAL INFORMATION:

APPLICANT: Emory University

TITLE OF INVENTION: Antithrombotic Variant Thrombins

FILE REFERENCE: B056 1070.1

CURRENT FILING DATE: 2002-06-07

NUMBER OF SEQ ID NOS: 13

SEQ ID NO: 1

LENGTH: 295

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE: CHAIN

NAME/KEY: (1)..  
(256)LOCATION: (1)..  
(256)

OTHER INFORMATION: Thrombin WE A-Chain

FEATURE: CHAIN

NAME/KEY: (37)..  
(295)LOCATION: (37)..  
(295)

OTHER INFORMATION: Thrombin WE B-Chain

US-10-165-442-3

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8e-11;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPDGKRGDACEGDSGGPFV 23

Db 224 AGYKPDGKRGDACEGDSGGPFV 246

RESULT 6 US-09-909-348A-6

Sequence 6, Application US/09909348A  
 Patent No. 6813416  
 1 AGYKPKDEGKGDAEGDGGPPFV 23

GENERAL INFORMATION:  
 APPLICANT: Carney, Darrell H.  
 APPLICANT: Crowther, Roger S.  
 APPLICANT: Stierenberg, Janet

TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN RECEPTOR

FILE REFERENCE: 3/033.1/003-001

CURRENT APPLICATION NUMBER: US/09/909,348A

CURRENT FILING DATE: 2001-07-19

PRIOR APPLICATION NUMBER: 60/219,800

PRIOR FILING DATE: 2000-07-20

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 6 LENGTH: 23

TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: peptide fragment of thrombin

NAME/KEY: AMIDATION at C-terminus  
 LOCATION: (23)..(23)  
 OTHER INFORMATION: Valine is Amidated

US-09-909-348A-6

RESULT 7 US-08-944-483-52

Query Match 100 0%; Score 131; DB 4; Length 23;  
 Best Local Similarity 100 0%; Pred. No. 3.8e-12; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGKGDAEGDGGPPFV 23

Db 1 AGYKPKDEGKGDAEGDGGPPFV 23

RESULT 8 US-10-165-442-2

Sequence 2, Application US/10165442  
 Patent No. 6706512

GENERAL INFORMATION:  
 APPLICANT: Emory University

TITLE OF INVENTION: Antithrombotic Variant Thrombins

FILE REFERENCE: E056.1070.1

CURRENT APPLICATION NUMBER: US/10/165,442

CURRENT FILING DATE: 2002-06-07

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patentin Version 3.0

SEQ ID NO 2 LENGTH: 259

TYPE: PRT  
 ORGANISM: Homo sapiens  
 FEATURE:  
 NAME/KEY: CHAIN  
 LOCATION: (1)..(259)  
 OTHER INFORMATION: Thrombin W215A B-Chain

US-10-165-442-2

Query Match 100.0%; Score 131; DB 4; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 5e-11; Mismatches 0; Indels 0; Gaps 0;

Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGYKPKDEGKGDAEGDGGPPFV 23

Db 1 AGYKPKDEGKGDAEGDGGPPFV 23

RESULT 9 US-10-165-442-4

Sequence 4, Application US/10165442  
 Patent No. 6705512

GENERAL INFORMATION:  
 APPLICANT: Emory University

TITLE OF INVENTION: Antithrombotic Variant Thrombins

FILE REFERENCE: E056.1070.1

CURRENT APPLICATION NUMBER: US/10/165,442

OM protein - protein search, using SW model  
Run on: March 31, 2005, 01:49:58 ; (without alignments)  
Scoring table: BLOSUM62 (54.786 Million cell updates/sec)

**Title:** US-10-766-752B-5  
**Perfect score:** 131  
**Sequence:** 1 AGYRDEGKRGDACEGSDGGPFV 23

**Scoring table:** Gapop 10.0 , Gapext 0.5  
**Searched:** 1407402 seqs, 331100923 residues

**Total number of hits satisfying chosen parameters:** 1407402  
**Minimum DB seq length:** 0  
**Maximum DB seq length:** 200000000

**Post-processing:** Minimum Match 0\*  
Maximum Match 100\*  
Listing first 45 summaries

**Database :** Published Applications AA:\*

1: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB.pep:\*

2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NW\_PUB.pep:\*

3: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*

4: /cgn2\_6/ptodata/2/pubpaa/US05\_PUBCOMB.pep:\*

5: /cgn2\_6/ptodata/2/pubpaa/US05\_NEW\_PUB.pep:\*

6: /cgn2\_6/ptodata/2/pubpaa/PCT05\_PUBCOMB.pep:\*

7: /cgn2\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep:\*

8: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

9: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB.pep:\*

10: /cgn2\_6/ptodata/2/pubpaa/US9B\_PUBCOMB.pep:\*

11: /cgn2\_6/ptodata/2/pubpaa/US9C\_PUBCOMB.pep:\*

12: /cgn2\_6/ptodata/2/pubpaa/US99\_NEW\_PUB.pep:\*

13: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

14: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

15: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

16: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

17: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

18: /cgn2\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep:\*

19: /cgn2\_6/ptodata/2/pubpaa/US10\_NEW\_PUB.pep:\*

20: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep:\*

**SUMMARIES**

Result No.	Score	Query Match Length	DB ID	Description
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2	131	100.0	23	9 US-09-904-090-3 Sequence 3, Appli
3	131	100.0	23	13 US-10-050-611-3 Sequence 3, Appli
4	131	100.0	23	13 US-10-050-611-4 Sequence 4, Appli
5	131	100.0	23	13 US-10-050-688-5 Sequence 5, Appli
6	131	100.0	23	13 US-10-050-688-6 Sequence 6, Appli
7	131	100.0	23	17 US-10-71-930-8 Sequence 8, Appli
8	131	100.0	259	11 US-09-788-210-2 Sequence 52, Appli
9	131	100.0	259	15 US-10-165-442-2 Sequence 2, Appli
10	131	100.0	259	15 US-10-165-442-4 Sequence 4, Appli
11	131	100.0	259	16 US-10-699-393-4 Sequence 2, Appli
12	131	100.0	259	16 US-10-699-393-4 Sequence 4, Appli
13	100.0	259	16 US-10-872-198-5 Sequence 5, Appli	

**Pred. No. 18** is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

```

; Patent No. US20020061852A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-001
; CURRENT APPLICATION NUMBER: US/09/904,090
; CURRENT FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: US 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Polypeptide, fragment of thrombin
; US-09-904-090-3

Query Match 100.0%; Score 131; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mis 0
Qy 1 AGYKPDGKRGDAECDGGGPV 23
Db 1 AGYKPDGKRGDAECDGGGPV 23

RESULT 3-US-050-611-3
; Sequence 3, Application US/1005611
; Publication No. US2002018793A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/217,583
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NO: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 3
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human fragment of thrombin
; US-10-050-611-3

Query Match 100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mis 0
Qy 1 AGYKPDGKRGDAECDGGGPV 23
Db 1 AGYKPDGKRGDAECDGGGPV 23

RESULT 4-US-10-050-611-4
; Sequence 4, Application US/1005611
; Publication No. US2002018793A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; TITLE OF INVENTION: METHODS OF THERAPY WITH THROMBIN DERIVED
; TITLE OF INVENTION: PEPTIDES
; FILE REFERENCE: 3033.1000-008
; CURRENT APPLICATION NUMBER: US/10/050,611
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/904,090
; PRIOR FILING DATE: 2000-07-12
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; US-10-050-611-4

Query Match 100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mis 0
Qy 1 AGYKPDGKRGDAECDGGGPV 23
Db 1 AGYKPDGKRGDAECDGGGPV 23

RESULT 5-US-10-050-688-5
; Sequence 5, Application US/1005688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.
; APPLICANT: Stieremberg, Janet
; APPLICANT: Bergman, John
; TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH
; TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN
; TITLE OF INVENTION: RECEPTOR
; FILE REFERENCE: 3033.1003-004
; CURRENT APPLICATION: 3033.1003-004
; CURRENT FILING DATE: 2002-01-16
; PRIOR APPLICATION NUMBER: 09/909,348
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: 60/219,800
; PRIOR FILING DATE: 2000-07-26
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 5
; LENGTH: 23
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide fragment of thrombin
; US-10-050-688-5

Query Match 100.0%; Score 131; DB 13; Length 23;
Best Local Similarity 100.0%; Pred. No. 1e-10; 0; Mismatches 0; Indels 0; Gaps 0;
Matches 23; Conservative 0; Mis 0
Qy 1 AGYKPDGKRGDAECDGGGPV 23
Db 1 AGYKPDGKRGDAECDGGGPV 23

RESULT 6-US-10-050-688-6
; Sequence 6, Application US/1005688
; Publication No. US20020198154A1
; GENERAL INFORMATION:
; APPLICANT: Carney, Darrell H.
; APPLICANT: Crowther, Roger S.

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APPLICANT: Stiernberg, Janet ; Publication No. US20040241646A1  
 APPLICANT: Bergmann, John ; GENERAL INFORMATION:  
 TITLE OF INVENTION: STIMULATION OF CARTILAGE GROWTH WITH  
 TITLE OF INVENTION: AGONISTS OF THE NON-PROTEOLYTICALLY ACTIVATED THROMBIN  
 PRIORITY REFERENCE: 3033-1003-004  
 CURRENT APPLICATION NUMBER: US/10/050,688  
 CURRENT FILING DATE: 2002-01-15  
 PRIOR APPLICATION NUMBER: 09/909,348  
 PRIOR FILING DATE: 2001-07-19  
 PRIOR APPLICATION NUMBER: 60/219,800  
 PRIOR FILING DATE: 2000-07-20  
 NUMBER OF SEQ ID NOS: 6  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 6  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial sequence  
 FEATURE: OTHER INFORMATION: peptide fragment of thrombin  
 FEATURE: NAME/KEY: AMIDATION  
 LOCATION: (23)..(23)  
 OTHER INFORMATION: CONNH2  
 .US-10-050-688-6

RESULT 7  
 US-10-718-930-9  
 ; Sequence 8, Application US/10718930  
 ; Publication No. US2005019331A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Garney, Darrell H.  
 ; APPLICANT: Ramakrishnan, Shyam  
 TITLE OF INVENTION: Synthetic Peptide Neutrophil Cell  
 TITLE OF INVENTION: Chemotactic Agents  
 FILE REFERENCE: 3033-1005-003  
 CURRENT APPLICATION NUMBER: US/10/718,930  
 CURRENT FILING DATE: 2003-11-20  
 PRIOR APPLICATION NUMBER: US 09/777,328  
 PRIOR FILING DATE: 2001-02-05  
 PRIOR APPLICATION NUMBER: US 08/330,594  
 NUMBER OF SEQ ID NOS: 9  
 SOFTWARE: FastSEQ for Windows Version 4.0  
 SEQ ID NO: 8  
 LENGTH: 23  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE: OTHER INFORMATION: Synthetic Peptide  
 .US-10-718-930-9

Query Match 100.0%; Score 131; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPPDEGKRGDAECDGGFPV 23  
 Db 1 AGYKPPDEGKRGDAECDGGFPV 23

RESULT 8  
 US-05-789-210-52  
 ; Sequence 52, Application US/09789210  
 ; Sequence 52, Application US/09789210

Query Match 100.0%; Score 131; DB 17; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 1.e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AGYKPPDEGKRGDAECDGGFPV 23  
 Db 1 AGYKPPDEGKRGDAECDGGFPV 23

RESULT 9  
 US-10-165-442-2  
 ; Sequence 2, Application US/10165442  
 ; Publication No. US20030215440A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Emory University  
 TITLE OF INVENTION: Antithrombotic Variant Thrombomina  
 FILE REFERENCE: E056 1070.1  
 CURRENT APPLICATION NUMBER: US/10/165,442  
 CURRENT FILING DATE: 2002-06-07  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: Patentin version 3.0  
 ; SEQ ID NO 2

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; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CHAIN
; LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin W215A B-Chain
US-10-165-442-2

Query Match 100.0%; Score 131; DB 15; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGYKDEDEGKGDAECDGSGGPV 23
Db 188 AGYKDEDEGKGDAECDGSGGPV 210

RESULT 10
US-10-165-442-4
; Sequence 4, Application US/10165442
; Publication No. US20030215440A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombins
; FILE REFERENCE: E036 1070.1
; CURRENT APPLICATION NUMBER: US/10/165,442
; CURRENT FILING DATE: 2002-06-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY:
LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin WE B-Chain
US-10-165-442-4

Query Match 100.0%; Score 131; DB 15; length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGYKDEDEGKGDAECDGSGGPV 23
Db 188 AGYKDEDEGKGDAECDGSGGPV 210

RESULT 11
US-10-699-393-2
; Sequence 2, Application US/10699393
; Publication No. US20040120943A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombin
; FILE REFERENCE: E036 1070.1
; CURRENT APPLICATION NUMBER: US/10/699,393
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY:
LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin WE B-Chain
US-10-699-393-2

Query Match 100.0%; Score 131; DB 15; length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AGYKDEDEGKGDAECDGSGGPV 23
Db 188 AGYKDEDEGKGDAECDGSGGPV 210

RESULT 12
US-10-699-393-4
; Sequence 4, Application US/10699393
; Publication No. US20040120943A1
; GENERAL INFORMATION:
; APPLICANT: Emory University
; TITLE OF INVENTION: Antithrombotic Variant Thrombin
; FILE REFERENCE: E036 1070.1
; CURRENT APPLICATION NUMBER: US/10/699,393
; CURRENT FILING DATE: 2003-10-31
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
SEQ ID NO 4
LENGTH: 259
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY:
LOCATION: (1)..(259)
; OTHER INFORMATION: Thrombin WE B-Chain
US-10-699-393-4

Query Match 100.0%; Score 131; DB 16; Length 259;
Best Local Similarity 100.0%; Pred. No. 1.1e-09; Length 259;
Qy
Db

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Best Local Similarity		100.0%	Pred. No.	1.1e-09;	Matches	23;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;		
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23		Qy	1	AGYKPDECKRGDACEGDSGGPFV	23		Qy	1	AGYKPDECKRGDACEGDSGGPFV	23			
Db	188	AGYKPDECKRGDACEGDSGGPFV	210		Db	224	AGYKPDECKRGDACEGDSGGPFV	246		Db	224	AGYKPDECKRGDACEGDSGGPFV	246			
GENERAL INFORMATION:																
APPLICANT:	Ulrich HAUPTS		APPLICANT:	Andre KOTTERMANN		APPLICANT:	Andreas SCHRIDIG		APPLICANT:	Christian VOTSMEIER		APPLICANT:	Ulrich KETTLING			
TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF																
FILE REFERENCE:	04156_0002U3		CURRENT APPLICATION NUMBER:	US/10/872,197A		CURRENT FILING DATE:	2004-06-18		PRIOR APPLICATION NUMBER:	60/524,960		PRIOR FILING DATE:	2003-11-25		PRIOR APPLICATION NUMBER:	EP 03025871
PRIOR FILING DATE:	2003-11-11		PRIOR APPLICATION NUMBER:	EP 03013819		PRIOR FILING DATE:	2003-11-10		NUMBER OF SEQ ID NOS:	96		SOFTWARE:	PatentIn version 3.1		SEQ ID NO:	5
LENGTH:	259		TYPE:	PRT		ORGANISM:	Homo sapiens		US-10-872-197A-5							
RESULT 14																
US-10-872-197A-5			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 15																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 16																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 17																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 18																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 19																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 20																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 21																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 22																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 23																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 24																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 25																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 26																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 27																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 28																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 29																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 30																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 31																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 32																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 33																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 34																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23													
Db	188	AGYKPDECKRGDACEGDSGGPFV	210													
RESULT 35																
US-10-165-442-1			Query Match	100.0%	Score	131;	DB	17;	Length	259;						
			Best Local Similarity	100.0%	Pred. No.	1.1e-09;			Mismatches	0;						
			Matches	23;	Indels	0;			Gaps	0;						
Qy	1	AGYKPDECKRGDACEGDSGGPFV	23					</td								

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